

SEQUENCE LISTING

<110> The Government of the United States of America, as represented by the Secretary, Department of Health and Human Services, c/o Centers for Disease Control and Prevention

Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of Flavivirus Infection

<130> 14114.0332P2

<150> 09/826,115

<151> 2001-04-04

<150> 09/701,536

<151> 2000-11-29

<150> PCT/US99/12298

<151> 1999-06-03

<150> 60/087,908

<151> 1998-06-04

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synthetic construct

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<222> (25)...(48)

<221> misc_feature

<222> 1-48

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48

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<223> Description of artificial sequence; note =
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Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
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gga gcc atg aag ttg tcg aat ttc cag ggg aag ctt ttg atg acc atc      1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
          30                35                40

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
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gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca      1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
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Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala	
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tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac	1383
Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn	
145 150 155	
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Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly	
160 165 170	
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Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu	
175 180 185	
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Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly	
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Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu	
205 210 215 220	
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Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro	
225 230 235	
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Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu	
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255 260 265	
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Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp	
270 275 280	
agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac	1815
Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn	
285 290 295 300	
gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc	1863
Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe	
305 310 315	
tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc	1911
Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile	
320 325 330	
aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac	1959
Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn	
335 340 345	

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Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr	
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Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys	
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<210> 11

<211> 697

<212> PRT

<213> Artificial Sequence

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<223> Description of artificial sequence; note =
synthetic construct

<223> pCDJE 2-7

<400> 11

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Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
35          40          45

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65					70					75				80	
Tyr	Glu	Cys	Pro	Lys	Leu	Thr	Met	Gly	Asn	Asp	Pro	Glu	Asp	Val	Asp
				85					90					95	
Cys	Trp	Cys	Asp	Asn	Gln	Glu	Val	Tyr	Val	Gln	Tyr	Gly	Arg	Cys	Thr
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Arg	Thr	Arg	His	Ser	Lys	Arg	Ser	Arg	Arg	Ser	Val	Ser	Val	Gln	Thr
			115				120					125			
His	Gly	Glu	Ser	Ser	Leu	Val	Asn	Lys	Lys	Glu	Ala	Trp	Leu	Asp	Ser
130						135					140				
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145					150					155					160
Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	Trp	Met	Leu	Gly
				165					170					175	
Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu	Leu	Leu	Leu	Val
			180					185					190		
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210						215					220				
Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro	Thr	Leu	Asp	Val
225					230					235					240
Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu	Val	Arg	Ser	Tyr
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Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val	Ala	Arg	Cys	Pro
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		275					280					285			
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Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	Lys	Tyr	Glu	Val
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Gly	Ile	Phe	Val	His	Gly	Thr	Thr	Thr	Ser	Glu	Asn	His	Gly	Asn	Tyr
			340					345					350		
Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	Thr	Val	Thr	Pro
			355				360					365			
Asn	Ala	Pro	Ser	Ile	Thr	Leu	Lys	Leu	Gly	Asp	Tyr	Gly	Glu	Val	Thr
			370			375					380				
Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	Ala	Phe	Tyr	Val
385					390					395					400
Met	Thr	Val	Gly	Ser	Lys	Ser	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	His
				405					410					415	
Asp	Leu	Ala	Leu	Pro	Trp	Thr	Ser	Pro	Ser	Ser	Thr	Ala	Trp	Arg	Asn
			420					425					430		
Arg	Glu	Leu	Leu	Met	Glu	Phe	Glu	Glu	Ala	His	Ala	Thr	Lys	Gln	Ser
			435				440						445		
Val	Val	Ala	Leu	Gly	Ser	Gln	Glu	Gly	Gly	Leu	His	Gln	Ala	Leu	Ala
			450				455				460				
Gly	Ala	Ile	Val	Val	Glu	Tyr	Ser	Ser	Ser	Val	Lys	Leu	Thr	Ser	Gly
465					470					475					480
His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Ala	Leu	Lys	Gly	Thr
				485					490					495	
Thr	Tyr	Gly	Met	Cys	Thr	Glu	Lys	Phe	Ser	Phe	Ala	Lys	Asn	Pro	Ala
			500					505					510		
Asp	Thr	Gly	His	Gly	Thr	Val	Val	Ile	Glu	Leu	Ser	Tyr	Ser	Gly	Ser
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Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
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 Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
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 Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
 565 570 575
 Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
 580 585 590
 Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
 595 600 605
 Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
 610 615 620
 Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
 625 630 635 640
 Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
 645 650 655
 Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
 660 665 670
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> misc_feature
 <222> 1-46
 <223> WN 466

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46

<210> 13
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<223> Description of artificial sequence; note =
synthetic construct

<223> JE Signal

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<210> 15

<211> 5308

<212> DNA

<213> Artificial Sequence

<220>

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<222> (911)...(2987)

<221> misc_feature

<222> (1)...(5308)

<223> pCBWN

<400> 15

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cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
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gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccggc	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420
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actgcttact	ggcttatcga	aattaatacg	actcactata	gggagaccca	agcttggtac	900
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	Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala					
	1 5 10					

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Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn	
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Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp	
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gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga	1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg	
50 55 60	

gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc	1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys	
65 70 75	
cca gtg ctg tgc gct ggt aat gat cca gaa gac atc gac tgt tgg tgc	1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys	
80 85 90	
aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc	1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg	
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cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa	1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu	
110 115 120 125	
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Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala	
130 135 140	
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga	1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly	
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tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc	1429
Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr	
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Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala	
175 180 185	
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Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly	
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Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys	
210 215 220	
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Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met	
225 230 235	
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg	1669
Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu	
240 245 250	
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga	1717
Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly	
255 260 265	
gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa	1765
Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln	
270 275 280 285	
gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa	1813
Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys	
290 295 300	

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Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile	
305 310 315	
gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt	1909
Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe	
320 325 330	
gtc cat gga cca act act gtg gag tgc cac gga aac tac tcc aca cag	1957
Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln	
335 340 345	
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Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro	
350 355 360 365	
tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt	2053
Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys	
370 375 380	
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt	2101
Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val	
385 390 395	
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Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn	
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ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg	2197
Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr	
415 420 425	
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Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala	
430 435 440 445	
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att	2293
Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile	
450 455 460	
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tgc ggt cat ttg	2341
Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu	
465 470 475	
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat	2389
Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr	
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ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca	2437
Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr	
495 500 505	
ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga	2485
Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly	
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cct tgc aaa gtt cct atc tgc tca gtg gct tca ttg aac gac cta acg	2533
Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr	
530 535 540	

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aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly 590 595 600 605	2725
gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser 610 615 620	2773
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<210> 16

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBWN

<400> 16

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 35          40          45
Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
 50          55          60
Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
 65          70          75          80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
 85          90          95
Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
100          105          110
Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
115          120          125
Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
130          135          140
Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145          150          155          160
Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
165          170          175
Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
180          185          190
Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
195          200          205
Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
210          215          220
Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
225          230          235          240

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Ser	Gly	Ile	Asp	Thr	Asn	Ala	Tyr	Tyr	Val	Met	Thr	Val	Gly	Thr	Lys	385	390	395
Thr	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	Met	Asp	Leu	Asn	Leu	Pro	Trp	405	410	415
Ser	Ser	Ala	Gly	Ser	Thr	Val	Trp	Arg	Asn	Arg	Glu	Thr	Leu	Met	Glu	420	425	430
Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Ser	Val	Ile	Ala	Leu	Gly	Ser	435	440	445
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Val	Lys	Met	Glu	Lys	Leu	Gln	Leu	Lys	Gly	Thr	Thr	Tyr	Gly	Val	Cys	485	490	495
Ser	Lys	Ala	Phe	Lys	Phe	Leu	Gly	Thr	Pro	Ala	Asp	Thr	Gly	His	Gly	500	505	510
Thr	Val	Val	Leu	Glu	Leu	Gln	Tyr	Thr	Gly	Thr	Asp	Gly	Pro	Cys	Lys	515	520	525
Val	Pro	Ile	Ser	Ser	Val	Ala	Ser	Leu	Asn	Asp	Leu	Thr	Pro	Val	Gly	530	535	540
Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Val	Ser	Val	Ala	Thr	Ala	Asn	Ala	545	550	555
Lys	Val	Leu	Ile	Glu	Leu	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Val	565	570	575
Val	Gly	Arg	Gly	Glu	Gln	Gln	Ile	Asn	His	His	Trp	His	Lys	Ser	Gly	580	585	590
Ser	Ser	Ile	Gly	Lys	Ala	Phe	Thr	Thr	Leu	Lys	Gly	Ala	Gln	Arg		595	600	605
Leu	Ala	Ala	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Val	Gly	Gly	610	615	620
Val	Phe	Thr	Ser	Val	Gly	Lys	Ala	Val	His	Gln	Val	Phe	Gly	Gly	Ala	625	630	635
Phe	Arg	Ser	Leu	Phe	Gly	Gly	Met	Ser	Trp	Ile	Thr	Gln	Gly	Leu	Leu	645	650	655
Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Ile	Asn	Ala	Arg	Asp	Arg	Ser	Ile	660	665	670
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<210> 17

<211> 5334

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (916)...(3007)

<221> misc_feature

<222> (1)...(5334)

<223> pCBE 1-14

<400> 17

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cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
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gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccggc	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccata	gggactttcc	420
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atgcccgata	catgacctta	tgggactttc	ctacttggca	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cggttttggc	agtacatcaa	tgggcgtgga	tagcggtttg	660
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aaaatcaacg	ggactttcca	aaatgtcgta	acaactccgc	cccattgacg	caaatgggcg	780
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ctgcttactg	gcttatcgaa	attaatacga	ctcactatag	ggagacccaa	gcttgggtacc	900
tctagagccg	ccgcc	atg ggc aga aag	caa aac aaa aga gga gga aat gaa			951
	Met Gly Arg Lys	Gln Asn Lys Arg Gly Gly Asn Glu				
	1	5	10			

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg	999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala	
15 20 25	

gga gcc atg aag ttg tgc aat ttc cag ggg aag ctt ttg atg acc atc	1047
Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile	
30 35 40	

aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga	1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly	
45 50 55 60	

gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag	1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu	
65 70 75	

gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca	1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro	
80 85 90	

gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat	1239
Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr	
95 100 105	

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tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala 125 130 135 140	1335
tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn 145 150 155	1383
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tgg atg ctt ggc agt aac aac ggt caa cgc gtg gta ttt acc atc ctc Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu 175 180 185	1479
ctg ctg ttg gtc gct ccg gct tac agt ttt aat tgt ctg gga atg ggc Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly 190 195 200	1527
aat cgt gac ttc ata gaa gga gcc agt gga gcc act tgg gtg gac ttg Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu 205 210 215 220	1575
gtg ctg gaa gga gat agc tgc ttg aca atc atg gca aac gac aaa cca Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro 225 230 235	1623
aca ttg gac gtc cgc atg att aac atc gaa gct agc caa ctt gct gag Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu 240 245 250	1671
gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val 255 260 265	1719
gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp 270 275 280	1767
agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn 285 290 295 300	1815
gga tgt gga ctt ttc ggg aag gga agc att gac aca tgt gca aaa ttc Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe 305 310 315	1863
tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile 320 325 330	1911
aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn 335 340 345	1959

cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe 350 355 360	2007
aca gta aca ccc aat gct cct tcg ata acc ctc aaa ctt ggt gac tac Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr 365 370 375 380	2055
gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu 385 390 395	2103
gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg 400 405 410	2151
gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr 415 420 425	2199
gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala 430 435 440	2247
aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His 445 450 455 460	2295
cag gcg ttg gca gga gcc atc gtg gtg gag tac tca agc tca gtg aag Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys 465 470 475	2343
tta aca tca ggc cac ctg aaa tgt agg ctg aaa atg gac aaa ctg gct Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala 480 485 490	2391
ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala 495 500 505	2439
aaa aat ccg gcg gac act ggt cac gga aca gtt gtc att gaa ctc tcc Lys Asn Pro Ala Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser 510 515 520	2487
tac tct ggg agt gat ggc ccc tgc aaa att ccg att gct tcc gtt gcg Tyr Ser Gly Ser Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala 525 530 535 540	2535
agc ctc aat gac atg acc ccc gtt ggg cgg ctg gtg aca gtg aac ccc Ser Leu Asn Asp Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro 545 550 555	2583
ttc gtc gcg act tcc agt gcc agc tca aag gtg ctg gtc gag atg gaa Phe Val Ala Thr Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu 560 565 570	2631
ccc ccc ttc gga gac tcc tac atc gta gtt gga agg gga gac aag cag Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln 575 580 585	2679

atc aac cac cat tgg cac aaa gct gga agc acg ctg ggc aag gcc ttt	2727
Ile Asn His His Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe	
590 595 600	
tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc gac aca	2775
Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr	
605 610 615 620	
gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa	2823
Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys	
625 630 635	
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga	2871
Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly	
640 645 650	
atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc tgg atg	2919
Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met	
655 660 665	
ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta gcc aca	2967
Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr	
670 675 680	
ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct t aattagtttg	3017
Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala	
685 690 695	
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<210> 18

<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBE 1-14

<400> 18

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20      25      30
Leu Ser Asn Phe Gln Gly Lys Leu Met Thr Ile Asn Thr Asp
35      40      45
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
50      55      60
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65      70      75      80
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
85      90      95
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
100     105     110
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
115     120     125
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
130     135     140
Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145     150     155     160
Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
165     170     175
Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Val
180     185     190
Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
195     200     205
Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
210     215     220
Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
225     230     235     240
Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
245     250     255
Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
260     265     270
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
275     280     285
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
290     295     300
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
305     310     315     320
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
325     330     335

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Gly	Ile	Phe	Val	His	Gly	Thr	Thr	Thr	Ser	Glu	Asn	His	Gly	Asn	Tyr	340	345	350
Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	Thr	Val	Thr	Pro	355	360	365
Asn	Ala	Pro	Ser	Ile	Thr	Leu	Lys	Leu	Gly	Asp	Tyr	Gly	Glu	Val	Thr	370	375	380
Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	Ala	Phe	Tyr	Val	385	390	395
Met	Thr	Val	Gly	Ser	Lys	Ser	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	His	405	410	415
Asp	Leu	Ala	Leu	Pro	Trp	Thr	Ser	Pro	Ser	Ser	Thr	Ala	Trp	Arg	Asn	420	425	430
Arg	Glu	Leu	Leu	Met	Glu	Phe	Glu	Glu	Ala	His	Ala	Thr	Lys	Gln	Ser	435	440	445
Val	Val	Ala	Leu	Gly	Ser	Gln	Glu	Gly	Gly	Leu	His	Gln	Ala	Leu	Ala	450	455	460
Gly	Ala	Ile	Val	Val	Glu	Tyr	Ser	Ser	Ser	Val	Lys	Leu	Thr	Ser	Gly	465	470	475
His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Ala	Leu	Lys	Gly	Thr	485	490	495
Thr	Tyr	Gly	Met	Cys	Thr	Glu	Lys	Phe	Ser	Phe	Ala	Lys	Asn	Pro	Ala	500	505	510
Asp	Thr	Gly	His	Gly	Thr	Val	Val	Ile	Glu	Leu	Ser	Tyr	Ser	Gly	Ser	515	520	525
Asp	Gly	Pro	Cys	Lys	Ile	Pro	Ile	Ala	Ser	Val	Ala	Ser	Leu	Asn	Asp	530	535	540
Met	Thr	Pro	Val	Gly	Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Val	Ala	Thr	545	550	555
Ser	Ser	Ala	Ser	Ser	Lys	Val	Leu	Val	Glu	Met	Glu	Pro	Pro	Phe	Gly	565	570	575
Asp	Ser	Tyr	Ile	Val	Val	Gly	Arg	Gly	Asp	Lys	Gln	Ile	Asn	His	His	580	585	590
Trp	His	Lys	Ala	Gly	Ser	Thr	Leu	Gly	Lys	Ala	Phe	Ser	Thr	Thr	Leu	595	600	605
Lys	Gly	Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	610	615	620
Gly	Ser	Ile	Gly	Gly	Val	Phe	Asn	Ser	Ile	Gly	Lys	Ala	Val	His	Gln	625	630	635
Val	Phe	Gly	Gly	Ala	Phe	Arg	Thr	Leu	Phe	Gly	Gly	Met	Ser	Trp	Ile	645	650	655
Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Val	Asn	Ala	660	665	670
Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	Ala	Thr	Gly	Gly	Val	Leu	675	680	685
Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala								690	695	

<210> 19

<211> 5283

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910) ... (2965)

<400> 19

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60

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cgagcaaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttagggtttag gcgtttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagtccat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc      360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
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atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgcccagta catgacctta tgggactttc ctacttgcca gtacatctac gtattagtca      600
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gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
      Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
            1             5             10

ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cgg gac      999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp
  15             20             25             30

agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc      1047
Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser
            35             40             45

cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg      1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met
            50             55             60

gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac      1143
Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp
            65             70             75

cag gag gaa gaa ccc gtt gac gtg gac tgc ttc tgc cga ggt gtt gat      1191
Gln Glu Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp
            80             85             90

agg gtt aag tta gag tat gga cgc tgt gga agg caa gct gga tct agg      1239
Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg
            95             100             105             110

ggg aaa agg tct gtg gtc att cca aca cat gca caa aaa gac atg gtc      1287
Gly Lys Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val
            115             120             125

ggg cga ggt cat gca tgg ctt aaa ggt gac aat att cga gat cat gtc      1335
Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val
            130             135             140

acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc      1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala
            145             150             155

att gtg gcc ttg gct tgg ctc atg gtt gat agt tgg atg gcc aga gtg      1431
Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val
            160             165             170

act gtc atc ctc ttg gcg ttg agt cta ggg cca gtg tac gcc acg agg      1479
Thr Val Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg
            175             180             185             190

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Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr	
210 215 220	
gct gag ggc aag cca tcc att gat gta tgg ctc gaa gac att ttt cag	1623
Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln	
225 230 235	
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Glu Ser Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr	
240 245 250	
aac aca aaa gtg gag gct cgc tgt cca acc act gga ccg gcg aca ctt	1719
Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu	
255 260 265 270	
ccg gag gag cat cag gct aat atg gtg tgc aag aga gac caa agc gac	1767
Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp	
275 280 285	
cgt gga tgg gga aac cac tgc ggg ttt ttt ggg aag ggc agt ata gtg	1815
Arg Gly Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val	
290 295 300	
gct tgt gca aag ttt gaa tgc gag gaa gca aaa aaa gct gtg ggc cac	1863
Ala Cys Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His	
305 310 315	
gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac	1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His	
320 325 330	
aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca	1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser	
335 340 345 350	
gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac	2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp	
355 360 365	
tat gga gat gtg tgc ctg acg tgt aaa gtg gca agt ggg att gat gtc	2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val	
370 375 380	
gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct	2103
Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro	
385 390 395	
tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc	2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro	
400 405 410	
tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg	2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val	
415 420 425 430	

gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly 435 440 445	2247
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gat gtg gga ctg gaa aag ctg aaa ctg aaa ggc aca acc tac tcc atg Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met 480 485 490	2391
tgt gac aaa gca aag ttc aaa tgg aag aga gtt cct gtg gac agc ggc Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly 495 500 505 510	2439
cat gac aca gta gtc atg gag gta tca tac aca gga agc gac aag cca His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro 515 520 525	2487
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gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly 545 550 555	2583
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gct gtg ggg gct ttg aca ctg atg atg aca atg gga gtt ggg gca t 2965
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 675 680 685

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<210> 20

<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<400> 20

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 20 25 30
 Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
 35 40 45

Val	Gly	Thr	Gly	Asn	Cys	Thr	Thr	Asn	Ile	Leu	Glu	Ala	Lys	Tyr	Trp
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Cys	Pro	Asp	Ser	Met	Glu	Tyr	Asn	Cys	Pro	Asn	Leu	Ser	Pro	Arg	Glu
65					70				75						80
Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	Val	Arg
				85				90						95	
Val	Ala	Tyr	Gly	Lys	Cys	Asp	Ser	Ala	Gly	Arg	Ser	Arg	Arg	Ser	Arg
			100					105					110		
Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	Thr	Arg
			115				120					125			
Gln	Glu	Lys	Trp	Met	Thr	Gly	Arg	Met	Gly	Glu	Arg	Gln	Leu	Gln	Lys
130						135					140				
Ile	Glu	Arg	Trp	Phe	Val	Arg	Asn	Pro	Phe	Phe	Ala	Val	Thr	Ala	Leu
145					150				155						160
Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	Val	Ile
				165				170						175	
Ala	Leu	Leu	Val	Leu	Ala	Val	Gly	Pro	Ala	Tyr	Ser	Ala	His	Cys	Ile
			180					185					190		
Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	Thr	Trp
			195				200					205			
Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	Ala	Pro
210						215					220				
Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	Asp	Arg
225					230					235					240
Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	His	Val
				245				250						255	
Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	Ala	Glu
			260					265					270		
Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	Arg	Gly
			275				280					285			
Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Val	Ala	Cys
290						295					300				
Ala	Lys	Phe	Thr	Cys	Ala	Lys	Ser	Met	Ser	Leu	Phe	Glu	Val	Asp	Gln
305					310					315					320
Thr	Lys	Ile	Gln	Tyr	Val	Ile	Arg	Ala	Gln	Leu	His	Val	Gly	Ala	Lys
				325				330						335	
Gln	Glu	Asn	Trp	Thr	Thr	Asp	Ile	Lys	Thr	Leu	Lys	Phe	Asp	Ala	Leu
			340					345					350		
Ser	Gly	Ser	Gln	Glu	Val	Glu	Phe	Ile	Gly	Tyr	Gly	Lys	Ala	Thr	Leu
			355				360					365			
Glu	Cys	Gln	Val	Gln	Thr	Ala	Val	Asp	Phe	Gly	Asn	Ser	Tyr	Ile	Ala
			370			375					380				
Glu	Met	Glu	Thr	Glu	Ser	Trp	Ile	Val	Asp	Arg	Gln	Trp	Ala	Gln	Asp
385					390					395					400
Leu	Thr	Leu	Pro	Trp	Gln	Ser	Gly	Ser	Gly	Gly	Val	Trp	Arg	Glu	Met
				405				410						415	
His	His	Leu	Val	Glu	Phe	Glu	Pro	Pro	His	Ala	Ala	Thr	Ile	Arg	Val
			420					425					430		
Leu	Ala	Leu	Gly	Asn	Gln	Glu	Gly	Ser	Leu	Lys	Thr	Ala	Leu	Thr	Gly
			435					440				445			
Ala	Met	Arg	Val	Thr	Lys	Asp	Thr	Asn	Asp	Asn	Asn	Leu	Tyr	Lys	Leu
					455					460					
His	Gly	Gly	His	Val	Ser	Cys	Arg	Val	Lys	Leu	Ser	Ala	Leu	Thr	Leu
465					470					475					480
Lys	Gly	Thr	Ser	Tyr	Lys	Ile	Cys	Thr	Asp	Lys	Met	Phe	Phe	Val	Lys
				485					490					495	
Asn	Pro	Thr	Asp	Thr	Gly	His	Gly	Thr	Val	Val	Met	Gln	Val	Lys	Val
			500					505					510		
Ser	Lys	Gly	Ala	Pro	Cys	Arg	Ile	Pro	Val	Ile	Val	Ala	Asp	Asp	Leu
			515				520					525			

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Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
530                    535                    540
Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
545                    550                    555                    560
Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
565                    570                    575
Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
580                    585                    590
Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
595                    600                    605
Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
610                    615                    620
Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
625                    630                    635                    640
Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
645                    650                    655
Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
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Met Phe Leu Ser Leu Gly Val Gly Ala
675                    680

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<210> 21

<211> 5304

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910)...(2986)

<400> 21

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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
gattattgac tagttattaa tagtaatcaa ttacgggggc attagttcat agcccatata      300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc      360
cccgccatt gagtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
attgacgtca atgggtggac tatttacggt aaactgcccc cttggcagta catcaagtgt      480
atcatatgcc aagtagcccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc      720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg      780
gtaggcggtg acggtgggag gtctatataa gcagagctct ctggctaact agagaacca      840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc      900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc      951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
1          5          10

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ttg gca gtt gtc ata gct ggt aca agc gct ttg cag tta tca acc tat      999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr
15          20          25          30

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cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc      1047
Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
35          40          45

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ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala	1095
50 55 60	
cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro	1143
65 70 75	
gtg ctt tca gcg gga aat gat ccc gag gac att gac tgt tgg tgt gac Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp	1191
80 85 90	
gtc gaa gag gtg tgg gtg cac tac gcc aga tgc acg cgc atg gga cat Val Glu Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His	1239
95 100 105 110	
tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser	1287
115 120 125	
aca ctg gca aca aag aac acg cca tgg ttg gac acc gtg aaa acc acc Thr Leu Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr	1335
130 135 140	
aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr	1383
145 150 155	
gcc cta gtt gcg ctg gcg att gga tgg atg ctc ggt agc aac aac aca Ala Leu Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr	1431
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cag aga gtg gtt ttt gtg atc atg ctg atg ctg att gct ccg gca tac Gln Arg Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr	1479
175 180 185 190	
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195 200 205	
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210 215 220	
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225 230 235	
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240 245 250	
acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu	1719
255 260 265 270	
gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp	1767
275 280 285	

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Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly	
290 295 300	
agc att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg	1863
Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly	
305 310 315	
aag acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg	1911
Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val	
320 325 330	
cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att	1959
His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile	
335 340 345 350	
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Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser	
355 360 365	
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Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu	
370 375 380	
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Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys	
385 390 395	
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Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu	
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cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg	2199
Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu	
415 420 425 430	
gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta	2247
Val Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu	
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gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca	2295
Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro	
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gcc act gtt agc agc tca acc cta acc ttg caa tca ggg cat ttg aaa	2343
Ala Thr Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys	
465 470 475	
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Cys Arg Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly	
480 485 490	
atg tgt gac tct gcc ttc acc ttc agc aag aac cca act gac aca ggg	2439
Met Cys Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly	
495 500 505 510	
cac ggg aca gtg att gtg gaa ctg cag tat act gga agc aac gga ccc	2487
His Gly Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro	
515 520 525	

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aac aac aag gtc atg atc gaa gtt gaa cca ccc ttt ggc gat tct tac Asn Asn Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr 560 565 570	2631
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cta ctt gga gct ctt ctc ctg tgg atg ggg ttg cag gcc cgc gac agg Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg 655 660 665 670	2919
agc atc tcg ctg act cta ctg gct gtc gga ggg att ctc atc ttt ctg Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu 675 680 685	2967
gca acc agc gtg caa gcc t gagcggccgc tcgagcatgc atctagaggg Ala Thr Ser Val Gln Ala 690	3016
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<210> 22

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 22

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Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
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Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
 35          40          45
Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
 50          55          60
Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
 65          70          75          80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
 85          90          95
Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
100          105          110
Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
115          120          125
Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
130          135          140
Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
145          150          155          160
Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
165          170          175
Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
180          185          190
Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
195          200          205
Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
210          215          220

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Met	Ala	Pro	Glu	Lys	Pro	Thr	Leu	Asp	Phe	Lys	Val	Met	Lys	Met	Glu	225	230	235	240
Ala	Thr	Glu	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Cys	Tyr	Glu	Ala	Thr	Leu	245	250	255	
Asp	Thr	Leu	Ser	Thr	Val	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	260	265	270	
Asn	Thr	Lys	Arg	Ser	Asp	Pro	Thr	Phe	Val	Cys	Lys	Arg	Asp	Val	Val	275	280	285	
Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	290	295	300	
Asp	Thr	Cys	Ala	Lys	Phe	Thr	Cys	Lys	Asn	Lys	Ala	Thr	Gly	Lys	Thr	305	310	315	320
Ile	Leu	Arg	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe	Val	His	Gly	325	330	335	
Ser	Thr	Asp	Ser	Thr	Ser	His	Gly	Asn	Tyr	Ser	Glu	Gln	Ile	Gly	Lys	340	345	350	
Asn	Gln	Ala	Ala	Arg	Phe	Thr	Ile	Ser	Pro	Gln	Ala	Pro	Ser	Phe	Thr	355	360	365	
Ala	Asn	Met	Gly	Glu	Tyr	Gly	Thr	Val	Thr	Ile	Asp	Cys	Glu	Ala	Arg	370	375	380	
Ser	Gly	Ile	Asn	Thr	Glu	Asp	Tyr	Tyr	Val	Phe	Thr	Val	Lys	Glu	Lys	385	390	395	400
Ser	Trp	Leu	Val	Asn	Arg	Asp	Trp	Phe	His	Asp	Leu	Asn	Leu	Pro	Trp	405	410	415	
Thr	Ser	Pro	Ala	Thr	Thr	Asp	Trp	Arg	Asn	Arg	Glu	Thr	Leu	Val	Glu	420	425	430	
Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Thr	Val	Val	Ala	Leu	Gly	Ser	435	440	445	
Gln	Glu	Gly	Ala	Leu	His	Thr	Ala	Leu	Ala	Gly	Ala	Ile	Pro	Ala	Thr	450	455	460	
Val	Ser	Ser	Ser	Thr	Leu	Thr	Leu	Gln	Ser	Gly	His	Leu	Lys	Cys	Arg	465	470	475	480
Ala	Lys	Leu	Asp	Lys	Val	Lys	Ile	Lys	Gly	Thr	Thr	Tyr	Gly	Met	Cys	485	490	495	
Asp	Ser	Ala	Phe	Thr	Phe	Ser	Lys	Asn	Pro	Thr	Asp	Thr	Gly	His	Gly	500	505	510	
Thr	Val	Ile	Val	Glu	Leu	Gln	Tyr	Thr	Gly	Ser	Asn	Gly	Pro	Cys	Arg	515	520	525	
Val	Pro	Ile	Ser	Val	Thr	Ala	Asn	Leu	Met	Asp	Leu	Thr	Pro	Val	Gly	530	535	540	
Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Ile	Ser	Thr	Gly	Gly	Ala	Asn	Asn	545	550	555	560
Lys	Val	Met	Ile	Glu	Val	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Val	565	570	575	
Val	Gly	Arg	Gly	Thr	Thr	Gln	Ile	Asn	Tyr	His	Trp	His	Lys	Glu	Gly	580	585	590	
Ser	Ser	Ile	Gly	Lys	Ala	Leu	Ala	Thr	Thr	Trp	Lys	Gly	Ala	Gln	Arg	595	600	605	
Leu	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Ile	Gly	Gly	610	615	620	
Val	Phe	Asn	Ser	Ile	Gly	Lys	Ala	Val	His	Gln	Val	Phe	Gly	Gly	Ala	625	630	635	640
Phe	Arg	Thr	Leu	Phe	Gly	Gly	Met	Ser	Trp	Ile	Thr	Gln	Gly	Leu	Leu	645	650	655	
Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Leu	Gln	Ala	Arg	Asp	Arg	Ser	Ile	660	665	670	
Ser	Leu	Thr	Leu	Leu	Ala	Val	Gly	Gly	Ile	Leu	Ile	Phe	Leu	Ala	Thr	675	680	685	
Ser	Val	Gln	Ala													690			

<210> 23
 <211> 5271
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> CDS
 <222> (910)...(2953)

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 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
 ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
 gattattgac tagttattaa tagtaatacaa ttacggggtc attagttcat agcccatata 300
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 ccgcgccatt gacgtcaata atgacgtatg ttcccatagt aacgccataa gggactttcc 420
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 tcgctattac catggtgatg cggtttttggc agtacatcaa tgggcgtgga tagcgggtttg 660
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 gccgcgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10
 ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999
 Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys
 15 20 25 30
 aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca 1047
 Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr
 35 40 45
 ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag 1095
 Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys
 50 55 60
 tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca 1143
 Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro
 65 70 75
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 Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn
 80 85 90
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 Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg
 95 100 105 110
 tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag 1287
 Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys
 115 120 125

acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc	1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu	
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caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg	1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr	
145 150 155	
gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc	1431
Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val	
160 165 170	
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Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His	
175 180 185 190	
tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga	1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly	
195 200 205	
act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg	1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met	
210 215 220	
gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att	1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile	
225 230 235	
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act	1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr	
240 245 250	
cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta	1719
His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu	
255 260 265 270	
gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat	1767
Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp	
275 280 285	
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Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val	
290 295 300	
gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt	1863
Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val	
305 310 315	
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg	1911
Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly	
320 325 330	
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat	1959
Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp	
335 340 345 350	
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct	2007
Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala	
355 360 365	

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atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc	2103
Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala	
385 390 395	
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Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg	
400 405 410	
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Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile	
415 420 425 430	
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Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu	
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act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac	2295
Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr	
450 455 460	
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Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu	
465 470 475	
aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt	2391
Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe	
480 485 490	
gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg	2439
Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val	
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Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp	
515 520 525	
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Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro	
530 535 540	
atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct	2583
Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro	
545 550 555	
ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act	2631
Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr	
560 565 570	
tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag	2679
Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln	
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acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg	2727
Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp	
595 600 605	

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His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn	
625 630 635	
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Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile	
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655 660 665 670	
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Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala	
675 680	
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atttccccga aaagtgccac ctgacgctc	5271

<210> 24

<211> 681
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<400> 24

Met	Gly	Lys	Arg	Ser	Ala	Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser	Leu	Ala	1	5	10	15
Val	Val	Ile	Ala	Gly	Thr	Ser	Ala	Val	Thr	Leu	Val	Arg	Lys	Asn	Arg	20	25	30	
Trp	Leu	Leu	Leu	Asn	Val	Thr	Ser	Glu	Asp	Leu	Gly	Lys	Thr	Phe	Ser	35	40	45	
Val	Gly	Thr	Gly	Asn	Cys	Thr	Thr	Asn	Ile	Leu	Glu	Ala	Lys	Tyr	Trp	50	55	60	
Cys	Pro	Asp	Ser	Met	Glu	Tyr	Asn	Cys	Pro	Asn	Leu	Ser	Pro	Arg	Glu	65	70	75	80
Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	Val	Arg	85	90	95	
Val	Ala	Tyr	Gly	Lys	Cys	Asp	Ser	Ala	Gly	Arg	Ser	Arg	Arg	Ser	Arg	100	105	110	
Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	Thr	Arg	115	120	125	
Gln	Glu	Lys	Trp	Met	Thr	Gly	Arg	Met	Gly	Glu	Arg	Gln	Leu	Gln	Lys	130	135	140	
Ile	Glu	Arg	Trp	Phe	Val	Arg	Asn	Pro	Phe	Phe	Ala	Val	Thr	Ala	Leu	145	150	155	160
Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	Val	Ile	165	170	175	
Ala	Leu	Leu	Val	Leu	Ala	Val	Gly	Pro	Ala	Tyr	Ser	Ala	His	Cys	Ile	180	185	190	
Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	Thr	Trp	195	200	205	
Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	Ala	Pro	210	215	220	
Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	Asp	Arg	225	230	235	240
Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	His	Val	245	250	255	
Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	Ala	Glu	260	265	270	
Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	Arg	Gly	275	280	285	
Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Val	Ala	Cys	290	295	300	
Ala	Lys	Phe	Thr	Cys	Ala	Lys	Ser	Met	Ser	Leu	Phe	Glu	Val	Asp	Gln	305	310	315	320
Thr	Lys	Ile	Gln	Tyr	Val	Ile	Arg	Ala	Gln	Leu	His	Val	Gly	Ala	Lys	325	330	335	
Gln	Glu	Asn	Trp	Thr	Thr	Asp	Ile	Lys	Thr	Leu	Lys	Phe	Asp	Ala	Leu	340	345	350	
Ser	Gly	Ser	Gln	Glu	Val	Glu	Phe	Ile	Gly	Tyr	Gly	Lys	Ala	Thr	Leu	355	360	365	
Glu	Cys	Gln	Val	Gln	Thr	Ala	Val	Asp	Phe	Gly	Asn	Ser	Tyr	Ile	Ala	370	375	380	
Glu	Met	Glu	Thr	Glu	Ser	Trp	Ile	Val	Asp	Arg	Gln	Trp	Ala	Gln	Asp	385	390	395	400
Leu	Thr	Leu	Pro	Trp	Gln	Ser	Gly	Ser	Gly	Gly	Val	Trp	Arg	Glu	Met	405	410	415	

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His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
    420                                425                                430
Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
    435                                440                                445
Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
    450                                455                                460
His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
    465                                470                                475                                480
Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
    485                                490                                495
Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
    500                                505                                510
Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
    515                                520                                525
Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
    530                                535                                540
Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
    545                                550                                555                                560
Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
    565                                570                                575
Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
    580                                585                                590
Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
    595                                600                                605
Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
    610                                615                                620
Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
    625                                630                                635                                640
Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
    645                                650                                655
Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
    660                                665                                670
Met Phe Leu Ser Leu Gly Val Gly Ala
    675                                680

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<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-35

<223> POW 454

<400> 25

aaaagaaaaa gcgctaccac catccaccgg gacag

35

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-41
<223> CPOW 2417

<400> 26
actgttaccc tcaaccccggt actcgccggc gaaaaagaaa a

41

<210> 27
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<223> Modified JE Signal

<400> 27
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15
Val Val Ile Ala Gly Thr Ser Ala
20

<210> 28
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-36
<223> YF 482

<400> 28
aaaagaaaaa gcgctgtgac cttggtgcgg aaaaac

36

<210> 29
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-41
<223> CYF 2433

<400> 29
acagagatcc tcaaccccggt actcgccggc gaaaaagaaa a

41

<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-41

<223> SLE 463

<400> 30

aaaagaaaaa gcgctttgca gttatcaacc tatcagggga a

41

<210> 31

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-40

<223> CSLE 2477

<400> 31

accgttggtc gcacgttcgg actcgccggc gaaaaagaaa

40

<210> 32

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 32

Leu	Asp	Thr	Ile	Asn	Arg	Arg	Pro	Ser	Lys	Lys	Arg	Gly	Gly	Thr	Arg
1				5				10						15	
Ser	Leu	Leu	Gly	Leu	Ala	Ala	Leu	Ile	Gly	Leu	Ala	Ser	Ser	Leu	Gln
			20					25					30		
Leu	Leu	Ser	Thr	Tyr	Gln	Gly									
			35												

<210> 33

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 33

Met	Trp	Leu	Ala	Ser	Leu	Ala	Val	Val	Ile	Ala	Cys	Ala	Gly	Ala	Met
1				5					10					15	
Lys	Leu	Ser	Asn	Phe	Gln	Gly	Lys								
			20												

<210> 34

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 34

Met	Asn	Glu	Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser	Leu	Ala	Val	Val	Ile
1				5					10					15	
Ala	Cys	Ala	Gly	Ala	Met	Lys	Leu	Ser	Asn	Phe	Gln	Gly	Lys		
			20				25						30		

<210> 35

<211> 39

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 35

Met	Gly	Arg	Lys	Gln	Asn	Lys	Arg	Gly	Gly	Asn	Glu	Gly	Ser	Ile	Met
1				5					10					15	
Trp	Leu	Ala	Ser	Leu	Ala	Val	Val	Ile	Ala	Cys	Ala	Gly	Ala	Met	Lys
			20				25						30		
Leu	Ser	Asn	Phe	Gln	Gly	Lys									
			35												

<210> 36

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 36

Met	Ser	Lys	Lys	Arg	Gly	Gly	Ser	Glu	Thr	Ser	Val	Leu	Met	Val	Ile
1				5					10					15	
Phe	Met	Leu	Ile	Gly	Phe	Ala	Ala	Ala	Leu	Lys	Leu	Ser	Asn	Phe	Gln
			20				25						30		
Gly	Lys														

<210> 37

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 37

Met	Gly	Lys	Arg	Ser	Ala	Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser	Leu	Ala
1				5					10					15	
Val	Val	Ile	Ala	Cys	Ala	Gly	Ala	Val	Thr	Leu	Ser	Asn	Phe	Gln	Gly
			20				25						30		
Lys															

<210> 38
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 38
Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn
1 5 10 15
Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile
20 25 30
Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu
35 40 45

<210> 39
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 39
Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp
1 5 10 15
Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala
20 25 30
Thr Val Arg Lys Glu Arg Gly Asp
35 40

<210> 40
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 40
Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala
1 5 10 15
Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 41
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 41

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Ile Ala Ala
 1 5 10 15
 Thr Val Arg Lys Glu Arg Gly Asp
 20

<210> 42
 <211> 5292
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> CDS
 <222> (910)...(2964)

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 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120
 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
 ttaggggttag gcgtttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
 tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
 cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccataa gggactttcc 420
 attgacgtca atgggtggag tatttacggg aaactgccca cttggcagta catcaagtgt 480
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
 atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600
 tcgctattac catggtgatg cggtttttggc agtacatcaa tgggcgtgga tagcggtttg 660
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780
 gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaacca 840
 ctgcttactg gcttatcgaa attaatagca ctcactatag ggagacccaa gcttggtacc 900
 gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10
 ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt 999
 Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
 15 20 25 30
 aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt 1047
 Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser
 35 40 45
 ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc 1095
 Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala
 50 55 60
 atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc 1143
 Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro
 65 70 75
 ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct 1191
 Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser
 80 85 90
 acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat 1239
 Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His
 95 100 105 110

aga	aga	gaa	aaa	aga	tca	gtg	gca	ctc	gtt	cca	cat	gtg	gga	atg	gga	1287
Arg	Arg	Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly	
				115					120					125		
ctg	gag	aca	cga	act	gaa	aca	tgg	atg	tca	tca	gaa	ggg	gcc	tgg	aaa	1335
Leu	Glu	Thr	Arg	Thr	Glu	Thr	Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys	
			130					135					140			
cat	gtc	cag	aga	att	gaa	act	tgg	atc	tgg	aga	cat	cca	ggc	ttc	acc	1383
His	Val	Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	
		145					150					155				
atg	atg	gca	gca	atc	ctg	gca	tac	acc	ata	gga	acg	aca	cat	ttc	caa	1431
Met	Met	Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	
	160					165					170					
aga	gcc	ctg	att	ttc	atc	tta	ctg	aca	gct	gtc	act	cct	tca	atg	aca	1479
Arg	Ala	Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr	
175					180					185					190	
atg	cgt	tgc	ata	gga	atg	tca	aat	aga	gac	ttt	gtg	gaa	ggg	gtt	tca	1527
Met	Arg	Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	
			195						200					205		
gga	gga	agc	tgg	gtt	gac	ata	gtc	tta	gaa	cat	gga	agc	tgt	gtg	acg	1575
Gly	Gly	Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr	
			210					215					220			
acg	atg	gca	aaa	aac	aaa	cca	aca	tgg	gat	ttt	gaa	ctg	ata	aaa	aca	1623
Thr	Met	Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	
		225					230					235				
gaa	gcc	aaa	cag	cct	gcc	acc	cta	agg	aag	tac	tgt	ata	gag	gca	aag	1671
Glu	Ala	Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	
	240					245					250					
cta	acc	aac	aca	aca	aca	gaa	tct	cgc	tgc	cca	aca	caa	ggg	gaa	ccc	1719
Leu	Thr	Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	
255					260					265					270	
agc	cta	aat	gaa	gag	cag	gac	aaa	agg	ttc	gtc	tgc	aaa	cac	tcc	atg	1767
Ser	Leu	Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	
			275						280					285		
gta	gac	aga	gga	tgg	gga	aat	gga	tgt	gga	cta	ttt	gga	aag	gga	ggc	1815
Val	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	
			290					295					300			
att	gtg	acc	tgt	gct	atg	ttc	aga	tgc	aaa	aag	aac	atg	gaa	gga	aaa	1863
Ile	Val	Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	
		305					310					315				
gtt	gtg	caa	cca	gaa	aac	ttg	gaa	tac	acc	att	gtg	ata	aca	cct	cac	1911
Val	Val	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	
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Ser	Gly	Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	
335					340					345					350	

gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr 355 360 365	2007
ggc tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp 370 375 380	2055
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val 385 390 395	2103
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala 400 405 410	2151
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe 415 420 425 430	2199
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln 435 440 445	2247
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met 450 455 460	2295
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg 465 470 475	2343
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly 480 485 490	2391
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile 495 500 505 510	2439
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro 515 520 525	2487
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aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555	2583
gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro 560 565 570	2631
gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln 575 580 585 590	2679

atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt	2727
Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly	
595 600 605	
gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata	2775
Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile	
610 615 620	
gga aag gct ctc cac caa gtc ttt gga gca atc tat gga gct gcc ttc	2823
Gly Lys Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe	
625 630 635	
agt ggg gtt tca tgg act atg aaa atc ctc ata gga gtc att atc aca	2871
Ser Gly Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr	
640 645 650	
tgg ata gga atg aat tca cgc agc acc tca ctg tct gtg aca cta gta	2919
Trp Ile Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val	
655 660 665 670	
ttg gtg gga att gtg aca ctg tat ttg gga gtc atg gtg cag gcc	2964
Leu Val Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala	
675 680 685	
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<210> 43
 <211> 685
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

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 35 40 45
 Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50 55 60
 Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
 65 70 75 80
 Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
 85 90 95
 Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
 100 105 110
 Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
 115 120 125
 Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
 130 135 140
 Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
 145 150 155 160
 Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
 165 170 175
 Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
 180 185 190
 Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
 195 200 205
 Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
 210 215 220
 Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
 225 230 235 240
 Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
 245 250 255
 Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
 260 265 270
 Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
 275 280 285
 Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
 290 295 300
 Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
 305 310 315 320
 Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
 325 330 335
 Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
 340 345 350
 Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
 355 360 365
 Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
 370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
 385 390 395 400
 Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
 405 410 415
 Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
 420 425 430
 Pro His Ala Lys Lys Gln Asp Val Val Leu Gly Ser Gln Glu Gly
 435 440 445
 Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
 450 455 460
 Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
 465 470 475 480
 Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
 485 490 495
 Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
 500 505 510
 Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
 515 520 525
 Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
 530 535 540
 Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
 545 550 555 560
 Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
 565 570 575
 Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
 580 585 590
 Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
 595 600 605
 Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
 610 615 620
 Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly
 625 630 635 640
 Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr Trp Ile
 645 650 655
 Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val Leu Val
 660 665 670
 Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
 675 680 685

<210> 44

<211> 5293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910)...(2964)

<400> 44

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cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
ttaggggttag	gcgttttgcg	ctgcttcgcg	atgtacgggc	cagatatacg	cgttgacatt	240
gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccgcg	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420
attgacgtca	atgggtggag	tatttacggg	aaactgccca	cttggcagta	catcaagtgt	480
atcatatgcc	aagtagccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540

atgccagta	catgacctta	tgggactttc	ctacttggca	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cggttttggc	agtacatcaa	tgggcgtgga	tagcggtttg	660
actcacgggg	atttccaagt	ctccacccca	ttgacgtcaa	tgggagtttg	ttttggcacc	720
aaaatcaacg	ggactttcca	aaatgtcgta	acaactccgc	cccattgacg	caaatgggcg	780
gtaggcgtgt	acggtgggag	gtctatataa	gcagagctct	ctggctaact	agagaaccca	840
ctgcttactg	gcttatcgaa	attaatacga	ctcactatag	ggagacccaa	gcttggtacc	900
gccgccgcc	atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc					951
	Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser					
	1	5		10		
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt						999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg						
15		20		25		30
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt						1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser						
	35		40			45
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc						1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala						
	50		55			60
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc						1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro						
	65		70			75
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct						1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser						
	80		85			90
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat						1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His						
	95		100			110
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga						1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly						
	115		120			125
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa						1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys						
	130		135			140
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc						1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr						
	145		150			155
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa						1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln						
	160		165			170
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca						1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr						
	175		180			185
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca						1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser						
	195		200			205
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg						1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr						
	210		215			220

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Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	
225 230 235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag	1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	
240 245 250	
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc	1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa	1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac	1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	
320 325 330	
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag	1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	
335 340 345 350	
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca	2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	
355 360 365	
ggg tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac	2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	
370 375 380	
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg	2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	
385 390 395	
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg	2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	
400 405 410	
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc	2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe	
415 420 425 430	
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa	2247
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln	
435 440 445	
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg	2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met	
450 455 460	

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atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly 480 485 490	2391
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile 495 500 505 510	2439
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro 515 520 525	2487
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile 530 535 540	2535
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555	2583
gca gaa cct cca ttc gga gac agc cac atc atc ata gga gta gag ccg Ala Glu Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro 560 565 570	2631
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atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly 595 600 605	2727
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gga aag gct ctc cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt Gly Lys Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe 625 630 635	2823
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tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu 655 660 665 670	2919
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala 675 680 685	2964
taattagttt gggcggccgc tcgagcatgc atctagaggc ccctattcta tagtgtcacc taaagtctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccattctgtg tttgcccttc ccccgtagct tccttgaccc tggaagggtg cactccact gtcctttcct aataaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctggggggtg gggtggggca ggacagcaag ggggaggatt gggaagacaa tagcaggcat gctgggggatg	3024 3084 3144 3204 3264

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<210> 45

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 45

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Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35          40          45
Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50          55          60
Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
 65          70          75          80
Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
 85          90          95
Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
100        105        110
Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
115        120        125

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Thr	Arg	Thr	Glu	Thr	Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys	His	Val
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Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	Met	Met
145					150					155					160
Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	Arg	Ala
				165					170					175	
Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr	Met	Arg
			180					185					190		
Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	Gly	Gly
	195					200						205			
Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr	Thr	Met
210					215						220				
Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	Glu	Ala
225					230					235					240
Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	Leu	Thr
				245					250					255	
Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	Ser	Leu
			260					265					270		
Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	Val	Asp
	275					280						285			
Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	Ile	Val
	290					295					300				
Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	Val	Val
305					310					315					320
Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	Ser	Gly
				325					330					335	
Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	Glu	Ile
			340					345					350		
Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	Gly	Tyr
	355						360					365			
Gly	Thr	Val	Thr	Met	Glu	Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Asn
	370					375					380				
Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	His	Arg
385					390					395					400
Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	Asp	Thr
				405					410					415	
Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	Lys	Asn
			420					425					430		
Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly
		435					440					445			
Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	Ser	Ser
	450					455					460				
Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	Met	Asp
465					470					475					480
Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly	Lys	Phe
				485					490					495	
Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile	Val	Ile
			500					505					510		
Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	Phe	Glu
		515					520					525			
Ile	Met	Asp	Leu	Glu	Lys	Arg	His	Val	Leu	Gly	Arg	Leu	Ile	Thr	Val
	530					535					540				
Asn	Pro	Ile	Val	Thr	Glu	Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu	Ala	Glu
545					550					555					560
Pro	Pro	Phe	Gly	Asp	Ser	His	Ile	Ile	Ile	Gly	Val	Glu	Pro	Gly	Gln
				565						570				575	
Leu	Lys	Leu	Asn	Trp	Phe	Lys	Lys	Gly	Ser	Ser	Ile	Gly	Gln	Met	Phe
			580					585					590		
Glu	Thr	Thr	Met	Arg	Gly	Ala	Lys	Arg	Met	Ala	Ile	Leu	Gly	Asp	Thr
		595					600					605			

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
 610 615 620
 Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
 625 630 635 640
 Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
 645 650 655
 Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
 660 665 670
 Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
 675 680 685

<210> 46

<211> 5293

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<221> CDS

<222> (910)...(2964)

<400> 46

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 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
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 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
 tggagttccg cgttacataa cttacggtaa atggccccgc tggctgaccg cccaacgacc 360
 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
 attgacgtca atgggtggac tatttacggt aaactgcca cttggcagta catcaagtgt 480
 atcatatgcc aagtagcggc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
 atgcccagta catgacctta tgggactttc ctacttgcca gtacatctac gtattagtca 600
 togtatttac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780
 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840
 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc 900
 gccgcggcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10

ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt 999
 Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
 15 20 25 30

aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt 1047
 Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser
 35 40 45

ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc 1095
 Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala
 50 55 60

atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc 1143
 Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro
 65 70 75

ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct	1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat	1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga	1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa	1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc	1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa	1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	
160 165 170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca	1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	
175 180 185 190	
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca	1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser	
195 200 205	
gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg	1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr	
210 215 220	
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca	1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	
225 230 235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag	1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	
240 245 250	
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc	1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa	1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	

gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His 320 325 330	1911
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys 335 340 345 350	1959
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr 355 360 365	2007
ggc tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp 370 375 380	2055
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val 385 390 395	2103
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala 400 405 410	2151
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe 415 420 425 430	2199
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln 435 440 445	2247
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met 450 455 460	2295
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aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile 495 500 505 510	2439
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro 515 520 525	2487
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile 530 535 540	2535
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555	2583

gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro 560 565 570	2631
gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys 575 580 585 590	2679
gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly 595 600 605	2727
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gga aaa gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe 625 630 635	2823
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tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu 655 660 665 670	2919
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala 675 680 685	2964
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<210> 47

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 47

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Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
 35          40          45
Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50          55          60
Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
 65          70          75          80
Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
 85          90          95
Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
100          105          110
Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
115          120          125
Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
130          135          140
Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
145          150          155          160
Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
165          170          175
Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
180          185          190
Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
195          200          205
Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
210          215          220
Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
225          230          235          240
Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
245          250          255
Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
260          265          270
Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
275          280          285
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
290          295          300
Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
305          310          315          320

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Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
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 Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
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 Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
 355 360 365
 Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
 370 375 380
 Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
 385 390 395 400
 Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
 405 410 415
 Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
 420 425 430
 Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
 435 440 445
 Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
 450 455 460
 Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
 465 470 475 480
 Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
 485 490 495
 Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
 500 505 510
 Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
 515 520 525
 Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
 530 535 540
 Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
 545 550 555 560
 Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
 565 570 575
 Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys Ala Phe
 580 585 590
 Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
 595 600 605
 Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
 610 615 620
 Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
 625 630 635 640
 Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
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 Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
 660 665 670
 Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
 675 680 685

<210> 48

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of artificial sequence; note =
 synthetic construct

<400> 48

tgtgcaggcg ccttccattht aaccacacgt aacg

34

<210> 49

<211> 40

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 49
tcgagcggcc gctcaactaa ttaggcctgc accatgactc

40

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 50
cttatcgaaa ttaatacgac tcactatagg

30

<210> 51
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 51
atagattgct ccaaacactt ggtgg

25

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 52
actccatagg aaaagccggt cacc

24

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 53
gcgagctcta gcatttaggt gacactatag

30

<210> 54
<211> 33
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 54

ctccaccaag tgtttggtgg tgccttcaga aca

33

<210> 55

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 55

Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr
1 5 10

<210> 56

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 56

cttatcgaaa ttaatacgac tcactatagg

30

<210> 57

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 57

gaattcgctc cacttccttt cttaaaccag ttgagcttc

39

<210> 58

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 58

ggaattcgtc tcggaagcac gctgggcaag g

31

<210> 59

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 59

gcgagctcta gcatttaggt gacactatag

30

<210> 60

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 60

aactggttta agaaaggaag cacgctgggc gcc

33

<210> 61

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 61

Asn Trp Lys Lys Gly Ser Thr Leu Gly Lys Ala

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